

### **Abstract**

The present invention is in the field of bioinformatics, particularly as it pertains to gene prediction. More specifically, the invention relates to the probabilistic analysis of nucleic acid sequences for the determination of coding features, including determination of state probabilities for each nucleotide in a nucleic acid sequence, determination of coding strand, determination of open reading frame extent, determination of insertion and deletion location, determination of exon location, and determination of protein sequence.